DATA SHEET Clariom D solutions

Clariom D solutions for human, mouse, and rat

Deep and broad transcriptome-level expression profiling solutions for a faster path to biomarker discovery

Accelerate your biomarker research with Applied Biosystems™ Clariom™ D solutions—the next generation of transcriptome-level profiling tools—providing a highly detailed view of the transcriptome for a faster path to biomarker discovery. Available for human, mouse, and rat, Clariom D solutions allow translational scientists to generate high-fidelity biomarker signatures quickly and easily with a design that provides intricate transcriptome-wide, gene- and exon-level expression profiles, including the ability to detect alternative splicing events of coding and long noncoding RNA, in a single three-day experiment.

Get all the data you need

- Rapidly identify complex disease signatures from as many as 540,000 transcripts, the most comprehensive coverage available, helping to ensure that biomarkers are not missed
- Confidently detect genes, exons, and alternative splicing events that give rise to coding and long noncoding RNA isoforms
- Detect rare and low-expressing transcripts otherwise missed by common sequencing practices
- Go from data to insight in minutes with intuitive, highly visual, free analysis software

Robust results even from precious samples

- Generate robust expression profiles from as little as 100 pg of total RNA—as few as 10 cells
- Use RNA from various sample types, including whole blood, cultured cells, and fresh/fresh-frozen or formalinfixed, paraffin-embedded (FFPE) tissues
- Preserve sample integrity and reduce data variability with an assay that does not require a globin or rRNA removal step

Clariom D solutions are available in a single-sample (cartridge array) format for use on the Applied Biosystems™ GeneChip™ 3000 instrument system and come with reagents and fast, simple Applied Biosystems™ Transcriptome Analysis Console (TAC) Software to analyze and visualize global expression patterns of genes, exons, pathways, and alternative splicing events.



Array specifications

Content summary	Human	Mouse	Rat	
Genes*	>134,700	>66,100	>68,900	
Transcripts*	>542,500	>214,900	>495,200	
Exons*	>948,300	>498,500	>320,400	
Exon-exon splice junctions*	>484,900	>282,500	>293,700	
Total probes*	>6,765,500	>6,022,300	>5,946,400	
Probes targeting exons*	>4,781,200	>4,895,600	>4,780,700	
Probes targeting exon- exon splice junctions*	>1,984,300	>1,126,700	>1,165,700	
Probe length (bases)	25	25	25	
Probe feature size	5 µm	5 μm	5 µm	
Background probes	Antigenomic set	Antigenomic set	Antigenomic set	

Performance specifications	Human, mouse, rat			
Total RNA input required**	100 pg-500 ng			
Sensitivity	≥1.5 pM			
Detectable 2-fold change	1:100,000 vs. 1:50,000			
Dynamic range	~3 logarithmic units			
Technical replicate signal correlation	≥0.90			
Correlation coefficient (intra-lot)	≥0.99			
cRNA yield	≥20 µg			
cDNA yield	≥6 µg			
Controls [†]	92 ERCC transcriptspoly(A) (dap, lys, phe, thr)			
Target orientation [‡]	Sense target			
Fluidics script	FS450_0001			

^{*} Numbers are representative of annotations as of April 2016. All numbers have been rounded down to the nearest hundred.

[‡] The probes tiled on the array are designed in the antisense orientation, requiring sense-strand, labeled targets to be hybridized to the array.

Data sources		Genes*			Transcripts*	
	Human	Mouse	Rat	Human	Mouse	Rat
Ensembl	>57,500	>37,600	>25,300	>196,000	>94,200	>28,500
VEGA	>48,500	>23,200	_	>176,700	>73,800	_
NONCODE	>55,900	>42,000	>500	>100,500	>67,300	>500
IncRNAWiki	>50,000	_	_	>99,900	_	_
UCSC Genes	>43,800	>26,300	_	>179,200	>54,400	_
AceView	>41,100	_	>30,900	>51,200	_	>59,400
miTranscriptome	>34,500	_	_	>74,600	_	_
RefSeq	>25,600	>23,500	>16,900	>50,800	>32,500	>18,100
MGC	>17,200	>17,400	>6,400	>26,000	>23,500	>6,600
MGI	_	>25,800	_	_	>33,000	_
RGD	_	_	>30,300	_	_	>62,000
Consensus CDS	>18,500	_	_	>30,400	_	_
RNA Central	>17,200	_	_	>27,900	_	_
circBase	>12,200	_	_	>90,800	_	_
Human Body Map	>10,200	_	_	>21,200	_	_
lincRNAdb	>80	>60	>10	>90	>80	>10
Nonoverlapping orthologous mouse gene and transcript models	_	_	>21,500	_	_	>28,100
Publication-specific gene sets**	>3,000	>10,000	>10,290	>6,000	>14,000	>17,320

^{*} Numbers are representative of annotations as of April 2016. All numbers have been rounded down to the nearest hundred.

^{**} Total RNA input requirements depend on assay selection. The assay types offered require different total RNA input amounts based on sample sources.

[†] Probe sets interrogating external RNA controls present in the Applied Biosystems™ ERCC RNA Spike-In Control Mixes (Cat. No. 4456740 and 4456739).

^{** 1.} Luo H, et al. (2013) Comprehensive characterization of 10,571 mouse large intergenic noncoding RNAs from whole transcriptome sequencing. PLoS One 8(8):e70835.

^{2.} Chalmel F, et al. (2014) High-resolution profiling of novel transcribed regions during rat spermatogenesis. Biol Reprod 91(1):5.

^{3.} Williams WP, et al. (2004) Increased levels of B1 and B2 SINE transcripts in mouse fibroblast cells due to minute virus of mice infection. Virology 327(2):233–241.

^{4.} Guo JU, et al. (2014) Expanded identification and characterization of mammalian circular RNAs. *Genome Biol* 15(7):409.



Ordering information

Quantity	Cat. No.
12 reactions	902924
30 reactions	902925
12 reactions	902663
30 reactions	902664
12 reactions	902665
30 reactions	902666
30 reactions	900720
10 reactions	902922
30 reactions	902923
10 reactions	902513
30 reactions	902514
10 reactions	902633
30 reactions	902634
30 reactions	900720
	30 reactions 12 reactions 30 reactions 12 reactions 30 reactions 30 reactions 10 reactions 10 reactions 10 reactions 30 reactions 30 reactions 30 reactions 30 reactions

